



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 151975

TO: Amy H Bowman
Location: REM-2C31&2C18
Art Unit: 1635
Wednesday, May 04, 2005

Case Serial Number: 10/605498

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

paul.schulwitz@uspto.gov

Search Notes

This Page Blank (uspto)

151975

From: Bowman, Amy
Sent: Thursday, April 28, 2005 12:54 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: 10/605,498

Hello,
I need a search of SEQ ID NO: 82 in application 10/605,498, length limited to 20 nucleobases. (I do not need any complements, just matches).
Thanks,
Amy Bowman
AU 1635
REM 2C18

ORFE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2005, 17:57:30 ; Search time 124 Seconds
(without alignments)
263.916 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 401682

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	65.0	20	3	US-09-046-858A-19
2	13	65.0	20	4	US-09-450-515-19
3	12.4	62.0	20	1	US-08-182-175A-9
4	12.4	62.0	20	1	US-08-474-633A-16
5	12.4	62.0	20	3	US-08-823-771-16
6	12.4	62.0	20	5	PCT-US92-06412-9
7	11.8	59.0	17	1	US-08-171-299B-6
8	11.8	59.0	20	3	US-09-467-642-13
9	11.6	58.0	18	4	US-09-402-618B-75
10	11.4	57.0	17	1	US-08-656-716-18
11	11.4	57.0	17	1	US-08-656-716-42
12	11.4	57.0	17	3	US-08-835-728D-18
13	11.4	57.0	17	3	US-08-835-728D-122
14	11.4	57.0	17	3	US-09-123-951-18
15	11.4	57.0	17	3	US-09-123-951-42
16	11.4	57.0	17	3	US-09-490-558-18
17	11.4	57.0	17	3	US-09-490-558-122
18	11	55.0	15	3	US-09-081-646-391
19	11	55.0	20	3	US-09-702-246-28
20	10.8	54.0	16	4	US-09-479-005A-5
21	10.8	54.0	17	1	US-08-171-299B-5
22	10.8	54.0	17	4	US-09-897-412-7
23	10.8	54.0	18	3	US-09-143-212-58
24	10.8	54.0	20	1	US-08-249-386A-15
25	10.8	54.0	20	2	US-08-478-178A-66
26	10.8	54.0	20	2	US-08-488-177-66
27	10.8	54.0	20	2	US-08-481-072A-66

28	10.8	54.0	20	2	US-08-664-336-66	Sequence 66, Appl
29	10.8	54.0	20	2	US-08-481-066A-66	Sequence 66, Appl
30	10.8	54.0	20	3	US-09-313-930-6	Sequence 6, Appl
31	10.8	54.0	20	3	US-08-829-637A-66	Sequence 66, Appl
32	10.8	54.0	20	4	US-10-025-139-66	Sequence 66, Appl
33	10.8	54.0	20	5	PCT-US95-06160-15	Sequence 15, Appl
34	10.6	53.0	18	3	US-09-218-979-31	Sequence 31, Appl
35	10.6	53.0	18	4	US-09-679-427-31	Sequence 31, Appl
36	10.6	53.0	18	4	US-09-402-618B-77	Sequence 77, Appl
37	10.6	53.0	18	4	US-09-402-618B-79	Sequence 79, Appl
38	10.6	53.0	18	4	US-09-220-536A-31	Sequence 31, Appl
39	10.6	53.0	20	1	US-08-050-073-173	Sequence 173, App
40	10.6	53.0	20	3	US-08-974-549A-477	Sequence 477, App
41	10.6	53.0	20	3	US-09-428-583-13	Sequence 13, Appl
42	10.6	53.0	20	4	US-08-912-951-244	Sequence 244, App
43	10.6	53.0	20	4	US-09-402-181B-477	Sequence 477, App
44	10.6	53.0	20	4	US-09-721-456-477	Sequence 477, App
45	10.4	52.0	14	1	US-08-373-124A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; TITLE OF INVENTION: IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046.858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-046-858A-19

Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACGCGCGCTCG 15
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Db 2 GACGGCGGCTCG 14

RESULT 2

US-09-450-515-19

; Sequence 19, Application US/09450515

; Patent No. 6680425

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond L.

; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES

; IN ALPHA-AMYLASE GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: PO Box 60850

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/450,515

; FILING DATE: 29-NO. 6680425-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/046,858

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Dehlinger, Peter J.

; REGISTRATION NUMBER: 28,006

; REFERENCE/DOCKET NUMBER: 2000-0456.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-0880

; TELEFAX: 650-324-0960

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-450-515-19

Query Match 65.0%; Score 13; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.1e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGGCGGCTCG 15

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Db 2 GACGGCGGCTCG 14

RESULT 3

US-08-182-175A-9

; Sequence 9, Application US/08182175A

; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,175A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..20

; OTHER INFORMATION: /product= "synthetic oligonucleotide"

; OTHER INFORMATION: /standard_name= "SM 70"

US-08-182-175A-9

Query Match 62.0%; Score 12.4; DB 1; Length 20;

Best Local Similarity 92.9%; Pred. No. 1.3e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGTC 18

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Db 7 CGCTGCGCTCGTC 20

RESULT 4

US-08-474-633A-16

; Sequence 16, Application US/08474633A

; Patent No. 5773691

; GENERAL INFORMATION:

; APPLICANT: E. I. DU PONT DE NEMOURS AND

; APPLICANT: COMPANY

; TITLE OF INVENTION: CHIMERIC GENES AND

; TITLE OF INVENTION: METHODS FOR INCREASING

; TITLE OF INVENTION: INCREASING THE LYSINE

; TITLE OF INVENTION: AND THREONINE CONTENT

; TITLE OF INVENTION: OF THE SEEDS OF PLANTS

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS

; ADDRESSEE: AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MICROSOFT WORD VERSION 2.0C

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,633A

; FILING DATE:

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/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..20
/ OTHER INFORMATION: /product= "synthetic
/ OTHER INFORMATION: oligonucleotide"
/ OTHER INFORMATION: /standard_name= "SM
/ OTHER INFORMATION: 70"
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US-08-474-633A-16

Query Match 62.0%; Score 12.4; DB 1; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGTC 18
DB 7 CGCTCGCTCGTC 20

RESULT 5
US-08-823-771-16
; Sequence 16, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; METHODS FOR INCREASING
; INCREASING THE LYSINE
; AND THREONINE CONTENT
;
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
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/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..20
/ OTHER INFORMATION: /product= "synthetic
/ OTHER INFORMATION: oligonucleotide"
/ OTHER INFORMATION: /standard_name= "SM
/ OTHER INFORMATION: 70"
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US-08-823-771-16

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGTC 18
DB 7 CGCTCGCTCGTC 20

RESULT 6
PCT-US92-06412-9
; Sequence 9, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9-August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..20
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OTHER INFORMATION: /product= "synthetic oligonucleotide"
OTHER INFORMATION: /standard_name= "SM 70"
PCT-US92-06412-9

Query Match 62.0%; Score 12.4; DB 5; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGGTC 18
DB 7 CGCTCGCTCGGTC 20

RESULT 7

US-08-171-299B-6/c

Sequence 6, Application US/08171299B
Patent No. 5599665

GENERAL INFORMATION:

APPLICANT: Barbieri, Joseph T.

APPLICANT: Frank, Dara W.

TITLE OF INVENTION: EXOZYME S PROTEIN PREPARATION AND CLONED EXOZYME S

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171,299B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 650053.90871

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5709

TELEFAX: (414) 271-3552

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other Nucleic Acid

US-08-171-299B-6

Query Match 59.0%; Score 11.8; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGG 16
DB 15 RGAGCGCGCTSGG 1

RESULT 8

US-09-467-642-13/c

Sequence 13, Application US/09467642

Patent No. 6300132

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRES

FILE REFERENCE: RTS-0106

CURRENT APPLICATION NUMBER: US/09/467,642

CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 13
LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-467-642-13

Query Match 59.0%; Score 11.8; DB 3; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGGTCA 19
DB 18 CGCGCGATCGGACA 4

RESULT 9

US-09-402-618B-75/c

Sequence 75, Application US/09402618B

Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotic

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patent In version 3.0

SEQ ID NO 75

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-402-618B-75

Query Match 58.0%; Score 11.6; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTCA 19
DB 18 GGGCCCGCGGCTGTCTCA 1

RESULT 10

US-08-656-716-18

Sequence 18, Application US/08656716

Patent No. 5786146

GENERAL INFORMATION:

APPLICANT: Herman, James G.

APPLICANT: Baylin, Stephen B.

TITLE OF INVENTION: METHYLATION SPECIFIC DETECTION

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/656,716
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/089001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-656-716-18

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGGCGCTCGGT 17
Db 3 CGCGGCGTTCGGT 15

RESULT 11
US-08-656-716-42/c
Sequence 42, Application US/08656716
Patent No. 5786146
GENERAL INFORMATION:
APPLICANT: Herman, James G.
APPLICANT: Baylin, Stephen B.
TITLE OF INVENTION: METHYLATION SPECIFIC DETECTION
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/089001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-656-716-42

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGGCGCTCGGT 17
Db 15 CGCGGCGTTCGGT 3

RESULT 12
US-08-835-728D-18
Sequence 18, Application US/08835728D
Patent No. 6017704
GENERAL INFORMATION:
APPLICANT: Herman, James G.
APPLICANT: Baylin, Stephen B.
TITLE OF INVENTION: Methylation Specific Detection
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: April 11, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,716
FILING DATE: June 03, 1996,
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/125001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-835-728D-18

Query Match 57.0%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGGCGCTCGGT 17
Db 3 CGCGGCGTTCGGT 15

RESULT 13
US-08-835-728D-122/c
Sequence 122, Application US/08835728D
Patent No. 6017704
GENERAL INFORMATION:
APPLICANT: Herman, James G.
APPLICANT: Baylin, Stephen B.

;; TITLE OF INVENTION: Methylation Specific Detection
;; NUMBER OF SEQUENCES: 216
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/835,728D
;; FILING DATE: April 11, 1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/656,716
;; FILING DATE: June 03, 1996,
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/125001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 122:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-835-728D-122

Query Match 57.0%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGGCGTTCGGT 17
DB 15 CGCGGCGTTCGGT 3

RESULT 14
US-09-123-951-18
; Sequence 18, Application US/09123951
; Patent No. 6200756
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: METHYLATION SPECIFIC DETECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,951
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,716

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/089001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-09-123-951-18

Query Match 57.0%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGGCGTTCGGT 17
DB 3 CGCGGCGTTCGGT 15

RESULT 15
US-09-123-951-42/c
; Sequence 42, Application US/09123951
; Patent No. 6200756
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: METHYLATION SPECIFIC DETECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,951
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/089001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-123-951-42

Query Match 57.0%; Score 11.4; DB 3; Length 17;

Best Local Similarity 92.3%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGGCGCTCGGT 17
|||||
Db 15 CGCGGCGCTCGGT 3

Search completed: May 3, 2005, 21:11:30
Job time : 126 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2005, 17:44:01 ; Search time 3014 Seconds
(without alignments)
252.583 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9.4	47.0	20	8	AZ961140
2	9.2	46.0	19	4	BM395903
3	9.2	46.0	20	1	AJ666384
4	9	45.0	19	8	AZ775541
5	9	45.0	20	7	CF281215
6	8.8	44.0	17	7	CF305567
7	8.8	44.0	18	8	BZ425195
8	8.8	44.0	19	1	AJ649246
9	8.8	44.0	19	8	AZ611716
10	8.8	44.0	20	8	AZ591658
11	8.6	43.0	20	4	BF966452
12	8.6	43.0	20	8	AZ992240
13	8.4	42.0	13	9	AJ594923
14	8.4	42.0	19	4	BM396331
15	8.4	42.0	19	7	CF542982
16	8.4	42.0	19	8	AZ610451
17	8.4	42.0	20	1	AJ801124
18	8.4	42.0	20	4	BM399952
19	8.4	42.0	20	8	AZ822878
20	8.2	41.0	14	5	BQ595292
21	8.2	41.0	15	4	BM399662
22	8.2	41.0	17	4	BM400706
23	8.2	41.0	18	4	BM400305
24	8.2	41.0	18	4	BM400816

C 25	8.2	41.0	19	8	AZ314110
C 26	8.2	41.0	19	8	AZ864551
C 27	8.2	41.0	20	4	BM401265
C 28	8.2	41.0	20	8	AZ591658
C 29	8	40.0	14	2	BE516032
C 30	8	40.0	19	1	AL042746
C 31	8	40.0	19	6	CA967213
C 32	8	40.0	19	8	AZ849133
C 33	8	40.0	20	2	AW250737
C 34	8	40.0	20	7	CF302285
C 35	8	40.0	20	8	AZ308410
C 36	8	40.0	20	8	AZ775705
C 37	8	40.0	20	9	AG194315
C 38	8	40.0	20	9	CL668826
C 39	7.8	39.0	14	1	AJ682145
C 40	7.8	39.0	15	1	AJ682954
C 41	7.8	39.0	15	2	AW246093
C 42	7.8	39.0	16	4	BM395715
C 43	7.8	39.0	16	7	CF303743
C 44	7.8	39.0	18	4	BM394214
C 45	7.8	39.0	18	4	BM394638

ALIGNMENTS

RESULT 1
AZ961140
LOCUS
DEFINITION 2M0229P20F Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0229P20 F, genomic survey sequence.
ACCESSION AZ961140
VERSION AZ961140.1 GI:13832367
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: P column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUC2M0229P20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 47.0%; Score 9.4; DB 8; Length 20;
Best Local Similarity 90.9%; Pred. No. 7.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGCGCTCGG 16
||| |||||
DB 8 GCTGGCGCTCGG 18

RESULT 2

BM395903 19 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-13-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395903
VERSION 1 GI:18195956
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

Location/Qualifiers
1..19
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 46.0%; Score 9.2; DB 4; Length 19;
Best Local Similarity 78.6%; Pred. No. 9.1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ACGGCGCTCGGT 17
||| |||||
DB 1 ACGGCGGCGGT 14

RESULT 3

BM395903
LOCUS 5009-0-13-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395903
VERSION 1 GI:18195956
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

Location/Qualifiers
1..20
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033 E03"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: BluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 46.0%; Score 9.2; DB 1; Length 20;
Best Local Similarity 78.6%; Pred. No. 9.1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACGCGCTCGT 15
||| |||||
DB 2 GGACCGGCTGACG 15

RESULT 4

AZ775541
LOCUS 2M0008H17F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC2M0008H17 F, genomic survey sequence.

ACCESSION AZ775541
VERSION 1 GI:12902185
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

AJ666384 20 bp mRNA linear EST 28-JUN-2004
LOCUS AJ666384 CSEQRAN09 Sus scrofa cDNA clone C0000033_E03, mRNA
DEFINITION sequence.

ACCESSION AJ666384
VERSION 1 GI:49350835
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector: pBluescriptII (KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

Location/Qualifiers
1..20
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033 E03"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 46.0%; Score 9.2; DB 1; Length 20;
Best Local Similarity 78.6%; Pred. No. 9.1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACGCGCTCGT 15
||| |||||
DB 2 GGACCGGCTGACG 15

RESULT 4

AZ775541
LOCUS 2M0008H17F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC2M0008H17 F, genomic survey sequence.

ACCESSION AZ775541
VERSION 1 GI:12902185
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: H column: 17

Seq primer: CGTTGTAAACGACGGCCGCT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. 19

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strains="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0008H17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 45.0%; Score 9; DB 8; Length 19;

Best Local Similarity 70.6%; Pred. No. 1.1e+07;

Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GGGACGGCGGCTCGGT 17

|||||

Db 1 GGGGGGGGGGCTCTGT 17

RESULT 5

CF281215/c

LOCUS

DEFINITION CF281215.1 20 bp mRNA linear EST 14-AUG-2003

14ETL--08-C23.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-C23,

mRNA sequence.

ACCESSION CF281215

VERSION CF281215.1 GI:33658602

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1. 20

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ETL--08-C23"

/tissue_type="callus"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CGCGCTCG 15

|||||

Db 16 CGCGCTCG 8

RESULT 6

CF305567

LOCUS

DEFINITION

CF305567

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF305567 17 bp mRNA linear EST 15-AUG-2003

HDA1--01-B07.g1 OshDACL-overexpressing transgenic rice lambda phage

cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA

clone HDA1--01-B07, mRNA sequence.

CF305567

CF305567.1 GI:33677328

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 17

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HDA1--01-B07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda

phage cDNA library I (HDA1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

rice Histone Deacetylase overexpression line."

ORIGIN

```

Query Match      44.0%; Score 8.8; DB 7; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.4e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGCGCGCT 13
   |||||
Db 2 GCACGAGCGCT 13

RESULT 7
BZ425195/c
LOCUS      BZ425195      18 bp      DNA      linear      GSS 13-DEC-2002
DEFINITION 100026548-5020 Aspergillus terreus random genomic DNA clone library
ACCESSION  BZ425195
VERSION    BZ425195.1 GI:26666650
KEYWORDS   GSS.
SOURCE     Aspergillus terreus
ORGANISM   Aspergillus terreus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
            Zimmer, D.P., Boers, W-E., Blomquist, P.R., Martinez, E.J.,
            Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,
            Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
            Madden, K.T.
TITLE      Integrating transcriptional and metabolite profiles to direct the
            engineering of lovastatin-producing strains
JOURNAL    Unpublished (2002)
COMMENT    Contact: Zimmer DP
            Microbia, Inc.
            One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
            Tel: 617-621-8322
            Fax: 617-
            Email: dzimmer@microbia.com
            Class: plasmid ends.

FEATURES             source
    source            1..18
                        /organism="Aspergillus terreus"
                        /mol_type="genomic DNA"
                        /strain="ATCC 20542 (A. terreus Thom, anamorph)"
                        /db_xref="taxon:33178"
                        /lab_host="Escherichia coli"
                        /clone_lib="Aspergillus terreus random genomic DNA clone
                        library"
                        /note="Vector: pZerOTM-2; Site_1: Sau3A; Site_2: BamHI;
                        Sau3A genomic fragments ligated into BamHI digested
                        pZerOTM-2"

ORIGIN
Query Match      44.0%; Score 8.8; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CGCGCTCGGTC 18
   |||||
Db 15 CCGAGCTCGTC 4

RESULT 8
AJ649246/c
LOCUS      AJ649246      19 bp      mRNA      linear      EST 07-JUL-2004
DEFINITION AJ649246 CSEQRAN19 Sus scrofa cDNA clone C0003271_p09, mRNA
            sequence.
ACCESSION  AJ649246
VERSION    AJ649246.1 GI:49326091
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 19)
            /organism="Sus musculus"

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS) R. Site1: EcoRI
R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
Location/Qualifiers
1..19
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003271_p09"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN
Query Match      44.0%; Score 8.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.4e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GGCGCTCGGTCA 19
   |||||
Db 19 GGCGCTCGGTCA 8

RESULT 9
AZ611716
LOCUS      AZ611716      19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0439B15F Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUGC1M0439B15 F, genomic survey sequence.
ACCESSION  AZ611716
VERSION    AZ611716.1 GI:11733906
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0438 row: B column: 15
            Seq primer: CGTTGTAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
            Location/Qualifiers
            1..19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0438B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 44.0%; Score 8.8; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.4e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GCGGCGCTCGGT 17
    |||||
Db 2 GCGGCGCGGCTT 13

RESULT 10
AZ591658/c
LOCUS 20 bp DNA linear GSS 13-DEC-2000
DEFINITION clone UUGC1M0401F19 R, genomic survey sequence.
ACCESSION AZ591658
VERSION AZ591658.1 GI:11713848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Seq primer: 0401 row: F column: 19
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/tissue_type="Mus musculus"

FEATURES
source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0401F19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 44.0%; Score 8.8; DB 8; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.4e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GCGGCGCTCGGT 17
    |||||
Db 20 GCAGCGCTGGGT 9

RESULT 11
BF966452
LOCUS 20 bp mRNA linear EST 23-JAN-2001
DEFINITION 602287066F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375648 5', mRNA sequence.
ACCESSION BF966452
VERSION BF966452.2 GI:12388052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
On Jan 16, 2001 this sequence version replaced gi:12333667.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10041 row: d column: 17
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
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FEATURES
source

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/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Query Match 43.0%; Score 8.6; DB 4; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+07;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGG 16
   ||| ||| ||| |||
Db 4 GGAGTCGGTCGCGG 18

RESULT 12
AZ992240/c
LOCUS 20276M15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0276M15 R, genomic survey sequence.
ACCESSION AZ992240.1 GI:13863467
VERSION AZ992240.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: M column: 15
Seq primer: CACACAGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC2M0276M15"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN
Query Match 43.0%; Score 8.6; DB 8; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+07;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCG 15
   ||| ||| ||| |||
Db 20 GGTACGCGGTGCTG 6

RESULT 13
AJ594923/c
LOCUS 13 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
408B05, genomic survey sequence.
ACCESSION AJ594923.1 GI:37944547
VERSION AJ594923.1
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelleier,G.,
Lepiniec,B., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 13)
AUTHORS Balzerque,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
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misc_feature 1..13
/notes="T-DNA flanking sequence
left border"

ORIGIN

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Query Match      42.0%; Score 8.4; DB 9; Length 13;
Best Local Similarity 90.0%; Pred. No. 2.2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CGCTCGGTCA 19
Db 13 CGCGCGGTCA 4

RESULT 14
BM396331/C
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-2-E02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396331
VERSION     BM396331.1 GI:18196384
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..19
/organism="Tetrahymena thermophila"
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
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Best Local Similarity 66.7%; Pred. No. 2.1e+07;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GACGCGCGCTCGGTTCAT 20
Db 19 GCCACCGCGGTGATCAT 2

RESULT 15
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DEFINITION S014680w-024-030-P12-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
clone 024-030-P12 5-PRIME, mRNA sequence.
ACCESSION  CF542982
VERSION     CF542982.1 GI:34891422
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

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TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 30 row: P column: 12
Seq primer: SP6.
Location/Qualifiers
1..19
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line)"
/db_xref="GABI:936786"
/db_xref="taxon:161934"
/clone="024-030-P12"
/tissue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pQWVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Query Match      42.0%; Score 8.4; DB 7; Length 19;
Best Local Similarity 90.0%; Pred. No. 2.1e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACGCGCGC 11
Db 2 GGACGCGCGG 11

Search completed: May 3, 2005, 21:09:19
Job time : 3021 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2005, 19:41:30 ; Search time 489 Seconds
(without alignments)
248.985 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcggcgtcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 1563430

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pubnpa/PCTUS PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubnpa/US08 NEW PUB.seq.*
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10: /cgn2_6/ptodata/2/pubnpa/US09B PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubnpa/US09C PUBCOMB.seq.*
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14: /cgn2_6/ptodata/2/pubnpa/US10B PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubnpa/US10C PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubnpa/US10D PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubnpa/US10E PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubnpa/US10F PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubnpa/US10 NEW PUB.seq.*
20: /cgn2_6/ptodata/2/pubnpa/US11 NEW PUB.seq.*
21: /cgn2_6/ptodata/2/pubnpa/US60 NEW PUB.seq.*
22: /cgn2_6/ptodata/2/pubnpa/US60 PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	18	US-10-605-498-82
2	19	95.0	19	18	US-10-605-498-90
3	13	65.0	20	14	US-10-206-654-19
4	12.6	63.0	20	17	US-10-131-827-8773
5	12.4	62.0	20	14	US-10-023-066A-16
6	12.4	62.0	20	18	US-10-804-678-16
7	11.8	59.0	19	15	US-10-198-677-20
8	11.8	59.0	20	17	US-10-148-355A-13
9	11.8	59.0	20	18	US-10-394-808-28
10	11.8	59.0	20	18	US-10-394-808-103
11	11.8	59.0	20	18	US-10-803-482-28
12	11.8	59.0	20	18	US-10-803-482-103
13	11.6	58.0	18	9	US-09-942-588A-31
14	11.6	58.0	18	9	US-09-764-420A-32
15	11.6	58.0	18	9	US-09-942-596A-31
16	11.6	58.0	18	10	US-09-988-873A-31
17	11.6	58.0	18	10	US-09-882-945A-75
18	11.6	58.0	18	10	US-09-942-662A-31
19	11.6	58.0	18	10	US-09-764-420A-32
20	11.6	58.0	18	14	US-10-231-302-31
21	11.6	58.0	18	17	US-10-608-804-31
22	11.6	58.0	18	17	US-10-634-510-31
23	11.6	58.0	18	18	US-10-807-114-75
24	11.6	58.0	18	19	US-10-655-362-75
25	11.6	58.0	20	10	US-09-888-361-147
26	11.4	57.0	13	17	US-10-391-415-20
27	11.2	56.0	16	18	US-10-712-672-1620
28	11.2	56.0	17	16	US-10-230-006-530
29	11.2	56.0	17	16	US-10-230-006-597
30	11.2	56.0	17	16	US-10-230-006-598
31	11.2	56.0	18	11	US-09-825-566-47
32	11.2	56.0	18	18	US-10-240-126-47
33	11.2	56.0	19	18	US-10-670-011-7
34	11.2	56.0	19	18	US-10-670-011-103
35	11.2	56.0	19	19	US-10-764-957-7
36	11.2	56.0	19	19	US-10-764-957-103
37	11.2	56.0	20	10	US-09-972-607-86
38	11.2	56.0	20	17	US-10-628-841-86
39	11.2	56.0	20	18	US-10-619-739-1280
40	11	55.0	19	17	US-10-016-490C-51
41	11	55.0	20	9	US-09-791-243-28
42	11	55.0	20	10	US-09-963-668B-9
43	11	55.0	20	14	US-10-096-595B-4
44	10.8	54.0	15	9	US-09-504-231A-926
45	10.8	54.0	15	9	US-09-274-553D-926

ALIGNMENTS

RESULT 1

US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-82

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTGTCAT 20

Db 1 GGGACGCGCGCTCGGTGTCAT 20

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RESULT 2
US-10-605-498-90/c
; Sequence 90, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.2
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-605-498-90

Query Match.          95.0%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGTGCAT 20
DB 19 GGACGGCGGCTCGTGCAT 1

RESULT 3
US-10-206-654-19
; Sequence 19, Application US/10206654
; Publication No. US2003003634A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/SOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match          65.0%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGGCGGCTCG 15
DB 2 GACGGCGGCTCG 14

RESULT 4
US-10-131-827-8773
; Sequence 8773, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773

Query Match          63.0%; Score 12.6; DB 17; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGTGCAT 20
DB 1 GTACGGCGTGTGGTGCAT 19

RESULT 5
US-10-023-066A-16
; Sequence 16, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE AND
; THREONINE CONTENT OF THE SEEDS OF
; PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..20
; OTHER INFORMATION: /product= "synthetic"
; oligonucleotide"
; /standard_name= "SM"
; 70"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
; US-10-023-066A-16
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; Query Match 62.0%; Score 12.4; DB 14; Length 20;
; Best Local Similarity 92.9%; Pred. No. 2.1e+04;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; QY 5 CGCGCGCTCGGTC 18
; DB 7 CGTGGCTCGGTC 20
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; RESULT 6
; US-10-804-678-16
; Sequence 16, Application US/10804678
; Publication No. US2005005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
;
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
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;
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNN M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..20
; OTHER INFORMATION: /product= "synthetic"
; oligonucleotide"
; /standard_name= "SM"
; 70"
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; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
; US-10-804-678-16
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; Query Match 62.0%; Score 12.4; DB 18; Length 20;
; Best Local Similarity 92.9%; Pred. No. 2.1e+04;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 5 CGCGCGCTCGGTC 18
; DB 7 CGTGGCTCGGTC 20
;
; RESULT 7
; US-10-198-677-20
; Sequence 20, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: KLUG, Aaron
; APPLICANT: MOORE, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; MOLECULES
; FILE REFERENCE: 8325-2011 / G11-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: bsG
;
; US-10-198-677-20
;
; Query Match 59.0%; Score 11.8; DB 15; Length 19;
; Best Local Similarity 86.7%; Pred. No. 4.1e+04;
; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 GGACGGCGGCTCGG 16
; DB 3 GGACGGCGGCTGGG 17
;
; RESULT 8
; US-10-148-355A-13/C
; Sequence 13, Application US/10148355A
; Publication No. US20030207831A1
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/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Lex M. Cowert
/ APPLICANT: ISIS PHARMACEUTICALS, INC.
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2
/ FILE REFERENCE: RTSP-0082
/ CURRENT APPLICATION NUMBER: US/10/148,355A
/ CURRENT FILING DATE: 2002-09-30
/ PRIOR APPLICATION NUMBER: 09/467,642
/ PRIOR FILING DATE: 1999-12-17
/ NUMBER OF SEQ ID NOS: 89
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-148-355A-13

Query Match      59.0%; Score 11.8; DB 17; Length 20;
Best Local Similarity 86.7%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGTCA 19
Db 18 CGCGGCGATCGACA 4

RESULT 9
US-10-394-808-28/c
/ Sequence 28, Application US/10394808
/ Publication No. US20040185559A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Mark J. Graham
/ TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 1 EXPRESSION
/ FILE REFERENCE: BIOL000303
/ CURRENT APPLICATION NUMBER: US/10/394,808
/ CURRENT FILING DATE: 2003-03-21
/ NUMBER OF SEQ ID NOS: 152
/ SEQ ID NO 28
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-394-808-28

Query Match      59.0%; Score 11.8; DB 18; Length 20;
Best Local Similarity 86.7%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCG 15
Db 20 GGGTCGCGCCCTCG 6

RESULT 10
US-10-394-808-103
/ Sequence 103, Application US/10394808
/ Publication No. US20040185559A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Mark J. Graham
/ TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 1 EXPRESSION
/ FILE REFERENCE: BIOL000303
/ CURRENT APPLICATION NUMBER: US/10/394,808
/ CURRENT FILING DATE: 2003-03-21
/ NUMBER OF SEQ ID NOS: 152
/ SEQ ID NO 103
/ LENGTH: 20
/ TYPE: RNA
/ ORGANISM: H. sapiens
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-394-808-103

Query Match      59.0%; Score 11.8; DB 18; Length 20;
Best Local Similarity 86.7%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCG 15
Db 20 GGGTCGCGCCCTCG 6

RESULT 11
US-10-803-482-28/c
/ Sequence 28, Application US/10803482
/ Publication No. US20040209838A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Mark J. Graham
/ TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 1 EXPRESSION
/ FILE REFERENCE: BIOL000303
/ CURRENT APPLICATION NUMBER: US/10/803,482
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: US 10/394,808
/ PRIOR FILING DATE: 2003-03-21
/ NUMBER OF SEQ ID NOS: 231
/ SEQ ID NO 28
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-803-482-28

Query Match      59.0%; Score 11.8; DB 18; Length 20;
Best Local Similarity 86.7%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCG 15
Db 20 GGGTCGCGCCCTCG 6

RESULT 12
US-10-803-482-103
/ Sequence 103, Application US/10803482
/ Publication No. US20040209838A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Mark J. Graham
/ TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 1 EXPRESSION
/ FILE REFERENCE: BIOL000303
/ CURRENT APPLICATION NUMBER: US/10/803,482
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: US 10/394,808
/ PRIOR FILING DATE: 2003-03-21
/ NUMBER OF SEQ ID NOS: 231
/ SEQ ID NO 103
/ LENGTH: 20
/ TYPE: RNA
/ ORGANISM: H. sapiens
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-803-482-103

Query Match      59.0%; Score 11.8; DB 18; Length 20;
Best Local Similarity 80.0%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCG 15
Db 1 GGGUCGCGGCCCTCG 15
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RESULT 15
US-09-942-596A-31
; Sequence 31, Application US/09942596A
; Patent No. US20020168648A1

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2005, 16:15:09 ; Search time 1802 Seconds
(without alignments)
537.794 Million cell updates/sec

Title: US-10-605-498-82

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
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12: gb_sy.*
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14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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c 2	19	95.0	19	6	CQ799992	CQ799992 Sequence
3	13	65.0	20	6	AR454276	AR454276 Sequence
4	12.4	62.0	20	6	AR014592	AR014592 Sequence
5	12.4	62.0	20	6	I26721	I26721 Sequence 9
6	12.4	62.0	20	6	AR235394	AR235394 Sequence
7	12.4	62.0	20	6	BD010384	BD010384 Chimeric
c 8	11.8	59.0	17	6	I34708	I34708 Sequence 6
9	11.8	59.0	19	6	AX202547	AX202547 Sequence
c 10	11.8	59.0	20	6	AR370192	AR370192 Sequence
11	11.6	58.0	18	6	BD133653	BD133653 Method fo
12	11.6	58.0	18	6	BD135731	BD135731 Method fo
13	11.6	58.0	18	6	BD160997	BD160997 Terminal-
14	11.6	58.0	18	6	BD167492	BD167492 A method
15	11.6	58.0	18	6	BD176975	BD176975 Method of
c 16	11.6	58.0	18	6	AR488746	AR488746 Sequence
17	11.6	58.0	18	6	AX391650	AX391650 Sequence
18	11.6	58.0	18	6	AX391799	AX391799 Sequence
c 19	11.6	58.0	18	6	AX419738	AX419738 Sequence

20	11.6	58.0	18	6	AX453807	AX453807 Sequence
21	11.6	58.0	18	6	BD000042	BD000042 Probe-cou
c 22	11.6	58.0	18	6	BD085000	BD085000 Target-de
23	11.6	58.0	20	6	AR271204	AR271204 Sequence
24	11.4	57.0	17	6	AR138777	AR138777 Sequence
c 25	11.4	57.0	17	6	AR138801	AR138801 Sequence
26	11.4	57.0	20	6	AX078038	AX078038 Sequence
c 27	11.2	56.0	17	6	AX760424	AX760424 Sequence
c 28	11.2	56.0	19	6	BD016694	BD016694 Method fo
29	11	55.0	15	6	AR180323	AR180323 Sequence
c 30	11	55.0	20	6	AR208819	AR208819 Sequence
31	11	55.0	20	6	AX412154	AX412154 Sequence
32	11	55.0	20	6	AX546229	AX546229 Sequence
33	10.8	54.0	15	6	BD208669	BD208669 Enzymatic
c 34	10.8	54.0	16	6	AR435746	AR435746 Sequence
c 35	10.8	54.0	17	6	I34707	I34707 Sequence 5
36	10.8	54.0	17	6	AR567813	AR567813 Sequence
37	10.8	54.0	17	6	AX348120	AX348120 Sequence
c 38	10.8	54.0	18	6	AR098803	AR098803 Sequence
c 39	10.8	54.0	20	6	AR037484	AR037484 Sequence
40	10.8	54.0	20	6	AR076701	AR076701 Sequence
41	10.8	54.0	20	6	AR153558	AR153558 Sequence
42	10.8	54.0	20	6	BD262873	BD262873 Antisense
43	10.8	54.0	20	6	BD272875	BD272875 Method of
44	10.8	54.0	20	6	AR182758	AR182758 Sequence
45	10.8	54.0	20	6	AR300838	AR300838 Sequence

ALIGNMENTS

RESULT 1
CQ799984
LOCUS CQ799984 Sequence 82 from Patent WO2004030660. linear PAT 28-APR-2004
DEFINITION CQ799984
ACCESSION CQ799984.1 GI:46848931
VERSION CQ799984.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 82 15-APR-2004;
The University of British Columbia (CA)
FEATURES
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/db_xref="taxon:9606"

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Db 1 GGGACGGCGCGCTCGGTCAAT 20

RESULT 2
CQ799992/c
LOCUS CQ799992 Sequence 90 from Patent WO2004030660. linear PAT 28-APR-2004
DEFINITION CQ799992
ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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seeds of plants.
ACCESSION BD010384
VERSION BD010384.1 GI:18638757
KEYWORDS JP 2001502923-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Falco,S.C., Iii,R.E.M. and Epelbaum,S.U.
TITLE Chimeric genes and methods for increasing the lysine content of the
JOURNAL seeds of plants
COMMENT Patent: JP 2001502923-A 16 06-MAR-2001;
EI DU PONT DE NEMOURS AND CO
OS Unidentified
PN JP 2001502923-A/16
PD 06-MAR-2001
PF 27-MAR-1998 JP 1998543284
PR 27-MAR-1997 US 08/824627
PI SAVERIO CARL FALCO,RAYMOND ERVIN MCDEVITT III, PI SABINE
URSULA EPELBAUM
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC
Strandedness: Single;
CC Topology: Linear;
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Best Local Similarity 92.9%; Pred. No. 1.2e+06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CGCGCGCGCTCGTC 18
Db 7 CGTCTCGCTCGTC 20
RESULT 8
I34708/c
LOCUS I34708 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 6 from patent US 5599665.
ACCESSION I34708
VERSION I34708.1 GI:2087676
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Barbieri,J.T., Frank,D.W. and Kulich,S.M.
TITLE Pseudomonas aeruginosa nucleic acids encoding exoenzyme S activity
and use thereof in detecting pseudomonas aeruginosa infection
JOURNAL Patent: US 5599665-A 6 04-FEB-1997;
FEATURES Location/Qualifiers
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Best Local Similarity 66.7%; Pred. No. 2.1e+06;
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Qy 2 GGACGCGCGCTCGG 16
Db 15 RGARGCGCTSGG 1
RESULT 9
I34708/c
LOCUS I34708 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 13 from patent US 6300132.
ACCESSION AR370192
VERSION AR370192.1 GI:34606698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Cowsert,L.M.
TITLE Antisense inhibition of telomeric repeat binding factor 2
expression
JOURNAL Patent: US 6300132-A 13 09-OCT-2001;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 59.0%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 CGCGCGCGCTCGTCA 19
Db 18 CGCGCGCATCGACA 4
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BD133653
LOCUS BD133653 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for screening mutated gene.
ACCESSION BD133653
VERSION BD133653.1 GI:23228598
KEYWORDS JP 2002071687-A/31.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
other sequences; artificial sequences.
AX202547
LOCUS AX202547 19 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 20 from Patent WO0153480.
ACCESSION AX202547
VERSION AX202547.1 GI:15392244
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Choo,Y., Klug,A. and Moore,M.T.
TITLE Nucleic acid binding polypeptides characterized by flexible linkers
connected nucleic acid binding modules
JOURNAL Patent: WO 0153480-A 20 26-JUL-2001;
Gendaq Limited (GB)
FEATURES Location/Qualifiers
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Db 3 GGACGCGCGCTTGG 17
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LOCUS AR370192 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 13 from patent US 6300132.
ACCESSION AR370192
VERSION AR370192.1 GI:34606698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Cowsert,L.M.
TITLE Antisense inhibition of telomeric repeat binding factor 2
expression
JOURNAL Patent: US 6300132-A 13 09-OCT-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 86.7%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 CGCGCGCGCTCGTCA 19
Db 18 CGCGCGCATCGACA 4
RESULT 11
BD133653
LOCUS BD133653 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for screening mutated gene.
ACCESSION BD133653
VERSION BD133653.1 GI:23228598
KEYWORDS JP 2002071687-A/31.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
other sequences; artificial sequences.
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AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Tanaka,S.
TITLE Method for screening mutated gene
JOURNAL Patent: JP 2002071687-A 31 12-MAR-2002;
COMMENT CANON INC
OS Artificial Sequence
PN JP 2002071687-A/31
PD 12-MAR-2002
PF 31-AUG-2000 JP 200263396
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,SHINYA TANAKA
PC G01N33/53,C12M1/00,C12N15/09,C12Q1/68,G01N31/22,G01N33/566, PC
G01N37/00,
PC C12N15/00
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1..18
Location/Qualifiers
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/db_xref='taxon:32630'
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Query Match 58.0%; Score 11.6; DB 6; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.6e+06;
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DB 1 GATGGGGCTCTCGTTCAT 18
RESULT 12
BD135731
LOCUS 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for detecting subjective component in specimen sample, and
ACCESSION BD135731
VERSION 1.1
KEYWORDS JP 2002065274-A/35.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.
TITLE Method for detecting subjective component in specimen sample, and
JOURNAL Patent: JP 2002065274-A 35 05-MAR-2002;
COMMENT CANON INC
OS Artificial Sequence
PN JP 2002065274-A/35
PD 05-MAR-2002
PF 31-AUG-2000 JP 200263395
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,AKIRA SHIMIZU
PC C12N15/09,C12M1/00,C12Q1/68,G01N31/22,G01N33/53, PC
G01N33/566,
PC G01N35/02,G01N37/00,C12N15/00,G01N35/06 CC DNA
probe for hybridizing with gene encoding
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Best Local Similarity 77.8%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GACGGGGCTCTCGTTCAT 20
DB 1 GATGGGGCTCTCGTTCAT 18
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BD160997
LOCUS 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Terminal-labeled probe-array and method for preparing it, and
ACCESSION BD160997
VERSION 1.1
KEYWORDS JP 2002153284-A/31.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto,T., Yamamoto,N. and Suzuki,T.
TITLE Terminal-labeled probe-array and method for preparing it, and
JOURNAL Patent: JP 2002153284-A 31 28-MAY-2002;
COMMENT CANON INC
OS Artificial Sequence
PN JP 2002153284-A/31
PD 28-MAY-2002
PF 24-NOV-2000 JP 2000357446
PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12Q1/68,G01N31/22,G01N33/53,G01N37/00, PC
C12N15/00
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FT /organism='Artificial Sequence'.
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Location/Qualifiers
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Query Match 58.0%; Score 11.6; DB 6; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 GACGGGGCTCTCGTTCAT 20
DB 1 GATGGGGCTCTCGTTCAT 18
RESULT 14
BD167492
LOCUS 18 bp DNA linear PAT 17-JAN-2003
DEFINITION A method of analyzing a base sequence of a nucleic acid.
ACCESSION BD167492
VERSION 1.1
KEYWORDS WO 0233068-A/31.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T. and Suzuki,T.
TITLE A method of analyzing a base sequence of a nucleic acid
JOURNAL Patent: WO 0233068-A 31 25-APR-2002;
COMMENT CANON KK,NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI
OS Artificial Sequence
PN WO 0233068-A/31
PD 25-APR-2002
PF 18-OCT-2000 WO 2000JP007244
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12Q1/68,G01N33/566,G01N33/53
CC Sample origonucleotide

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Best Local Similarity 77.8%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 GATGGGGCTCTCGTTCAT 18
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BD176975 18 bp DNA linear PAT 16-APR-2003
LOCUS
DEFINITION Method of analyzing nucleic acid base sequence.
ACCESSION BD176975
VERSION BD176975.1 GI:30014234
KEYWORDS JP 2002306166-A/31.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 18)
Yamamoto, N., Okamoto, H. and Suzuki, T.
METHOD OF ANALYZING NUCLEIC ACID BASE SEQUENCE
TITLE Patent: JP 2002306166-A 31 22-OCT-2002;
JOURNAL CANON INC
COMMENT
OS Artificial Sequence
PN JP 2002306166-A/31
PD 22-OCT-2002
PF 31-AUG-2000 JP 2000263506
PI NOBUKO YAMAMOTO, HISASHI OKAMOTO, TOMOHIRO SUZUKI PC
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Best Local Similarity 77.8%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 GATGGGGCTCTCGTTCAT 18
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2005, 16:10:24 ; Search time 422 Seconds
(without alignments)
280.556 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcggcctcggtcat 20

Scoring table: IDENTITY_NUC

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2207178

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	12 ADM94732	Adm94732 Human hea
2	19	95.0	19	12 ADM94740	Adm94740 Human hea
3	12.6	63.0	20	6 ABZ08781	Abz08781 Human CMV
4	12.4	62.0	19	3 AAA40594	Aaa40594 Human Arp
5	12.4	62.0	20	2 AQC36810	Aqc36810 Oligomer
6	12.4	62.0	20	2 AQC94968	Aqc94968 PCR prime
7	12.4	62.0	20	2 AAV35805	Aav35805 PCR prime
8	12.4	62.0	20	2 AAV95501	Aav95501 Plasmid p
9	12.4	62.0	20	8 ADA16031	Ada16031 Plasmid p
10	12.4	62.0	20	9 ACH03677	Ach03677 Plasmid p
11	12.4	62.0	20	10 ADF73001	Adf73001 Probe rel
12	11.8	59.0	15	6 AAD26768	Aad26768 Human SNA
13	11.8	59.0	17	2 AAT61840	Aat61840 Pseudomon
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15	11.8	59.0	20	5 AAH20644	Aah20644 Human tel
16	11.8	59.0	20	10 ABZ87221	Abz87221 Human oli
17	11.8	59.0	20	11 ABD23451	Abd23451 Human myo
18	11.8	59.0	20	13 ADS00264	Ads00264 Human dia
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	23	11.6	58.0	18	6	ABK72469	Abk72469 Sample or
	24	11.6	58.0	18	6	ABN99777	Abn99777 DNA probe
	25	11.6	58.0	18	6	ABL54931	Ab154931 Human tum
	26	11.6	58.0	18	6	ABL46108	Ab146108 Mycobacte
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	28	11.6	58.0	18	6	ABL59666	Ab159666 Oligonuc1
	29	11.6	58.0	18	6	ABT06245	Abt06245 Synthetic
c	30	11.6	58.0	18	12	ADK82298	Adk82298 Mycobacte
	31	11.6	58.0	20	4	AAH22265	Aah22265 Fibroblas
	32	11.6	58.0	20	10	ADC65851	Adc65851 Mouse TGF
c	33	11.6	58.0	20	10	ABZ98678	Abz98678 Human try
	34	11.6	58.0	20	10	ABZ87769	Abz87769 Human oli
c	35	11.6	58.0	20	11	ABD31709	Abd31709 Human try
	36	11.6	58.0	20	11	ABD23999	Abd23999 Human cal
	37	11.6	58.0	20	12	ADJ60557	Adj60557 Oligonuc1
c	38	11.6	58.0	20	12	ADO46046	Ado46046 Human oli
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c	41	11.4	57.0	15	6	ABK95806	Abk95806 Solute Ca
	42	11.4	57.0	15	6	AB199079	Ab199079 Human PCD
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	44	11.4	57.0	17	2	AAV09425	Aav09425 CpG-conta
c	45	11.4	57.0	17	12	ADQ78137	Adq78137 PCR prime

ALIGNMENTS

RESULT 1

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AC	ADM94732;	
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DT	01-JUL-2004	(first entry)
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DE	Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.	
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KW	heat shock protein 27; hsp27; cytostatic; gene therapy;	
KW	heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;	
KW	antisense oligonucleotide; ss.	
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OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO2004030660-A2.	
XX		
PD	15-APR-2004.	
XX		
PF	02-OCT-2003; 2003WO-CA001588.	
XX		
PR	02-OCT-2002; 2002US-0415859P.	
PR	18-APR-2003; 2003US-0463952P.	
XX		
PA	(UYBR-) UNIV BRITISH COLUMBIA.	
XX		
PI	Gleave ME, Rocchi P, Signaevsky M;	
XX		
DR	WPI; 2004-316331/29.	
XX		
PT	New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous system malignancy.	
PT	Claim 6; SEQ ID NO 82; 38pp; English.	
PS	The present invention describes a composition which comprises a	
CC	therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The composition has cytostatic activity, and can be used in gene therapy.	
CC		

CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCGGTTCAT 20
DB 1 GGGACGGCGCTCGGTTCAT 20

RESULT 2
ADM94740/c
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AC ADM94740;
XX
XX
DT 01-JUL-2004 (first entry)
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DE Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.
XX
XX heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW short interfering RNA; siRNA; RNA interference; RNAi; ds.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004030660-A2.
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PD 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-CA001588.
PF
XX 02-OCT-2002; 2002US-0415959P.
PR
XX 18-APR-2003; 2003US-0463952P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Gleave ME, Rocchi P, Signaevsky M;
PI
XX WPI; 2004-316331/29.
XX
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
XX Claim 10; SEQ ID NO 90; 38pp; English.
PS
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACGGCGCTCGGTTCAT 20

DB 19 GGGACGGCGCTCGGTTCAT 1

RESULT 3
ABZ08781
ID ABZ08781 standard; DNA; 20 BP.
XX
AC ABZ08781;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human CMV PCR primer SEQ ID NO 8773.
XX
XX CMV; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; PCR;
KW primer; ss.
XX
XX Human cytomegalovirus.
OS
XX WO200257414-A2.
PN
XX 25-JUL-2002.
PD
XX 22-OCT-2001; 2001WO-US047856.
PF
XX 20-OCT-2000; 2000US-0241994P.
PR
XX 08-JUN-2001; 2001US-0296764P.
PR
XX (BIOC-) BIOCARDIA INC.
PA
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quattermost T, Johnson F;
PI
XX WPI; 2002-636525/68.
DR
XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Example 18; Page 142; Opp; English.
PS
XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The
CC present sequence is that of a CMV PCR primer used in the invention
XX
SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGACGGCGCTCGGTTCAT 20
DB 1 GTACGGCTGCTGGGTTCAT 19

RESULT 4
AAA40594/c
ID AAA40594 standard; DNA; 19 BP.
XX
XX AAA40594;
AC

```

XX 20-NOV-2000 (first entry)
XX Human Arp3H PCR primer #1.
XX Human; Arp3H; actin-related protein; PCR primer; amplification; ss.
XX Homo sapiens.
XX CN1252448-A.
XX 10-MAY-2000.
XX 22-OCT-1998; 98CN-00123482.
XX 22-OCT-1998; 98CN-00123482.
XX (XINH-) XINHUANGFU FUDAN GENE ENG CO LTD SHANGHA.
XX Yu L, Fu Q, Zhang H;
XX WPI; 2000-443229/39.
XX Human actin related protein gene and encoded polypeptide preparation.
XX Example 1; Page 17; 25pp; Chinese.
XX This invention describes a novel preparation which provides a new human
XX Arp3H as an actin-related protein gene family member. The present
XX invention provides the cDNA sequence of the actin related protein gene
XX and the polypeptide encoded by the said sequence, as well as the
XX recombination technology to produce the actin related protein gene. This
XX sequence represents a PCR primer used in the amplification of the human
XX Arp3A gene described in the method of the invention
XX
XX Query Match 62.0%; Score 12.4; DB 3; Length 19;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+04;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5 CGCGGCGCTCGGTC 18
XX |||||
XX 17 CGCGGCGCTCGGCC 4
XX
XX RESULT 5
XX ID AAQ36810 standard; DNA; 20 BP.
XX AC AAQ36810;
XX 25-MAR-2003 (revised)
XX 22-JUN-1993 (first entry)
XX Oligomer SM 70 used in construction of SSP polypeptides.
XX Heptad; plants; custom tailored storage proteins; in vivo; expression;
XX ss.
XX Synthetic.
XX WO9303160-A1.
XX 18-FEB-1993.
XX 07-AUG-1992; 92WO-US006412.
XX 09-AUG-1991; 91US-00743006.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Keeler SJ, Rice JA;
XX
XX Query Match 62.0%; Score 12.4; DB 2; Length 20;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+04;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5 CGCGGCGCTCGGTC 18
XX |||||
XX 7 CGCTGCGCTCGGTC 20
XX
XX RESULT 6
XX ID AAQ94968 standard; DNA; 20 BP.
XX AC AAQ94968;
XX 15-JUL-1996 (first entry)
XX PCR primer SM 70.
XX Lysine; synthetic storage protein; SSP; vector; pSK6;
XX dihydridipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX Glycine max; rapeseed; oilseed rape; Brassica napus; transgenic plant;
XX essential amino acid; primer; PCR; polymerase chain reaction; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_feature 1..20
XX /*tag= a
XX /standard_name= "SM 70"
XX
XX WO9515392-A1.
XX 08-JUN-1995.
XX 21-NOV-1994; 94WO-US013190.
XX 30-NOV-1993; 93US-00160117.
XX 17-JUN-1994; 94US-00261661.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Keeler SJ, Rice JA;
XX WPI; 1995-215272/28.
XX
XX New chimeric gene providing increased lysine content in plant seeds -
XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX transport sequence and seed specific promoter, also new plants of
XX improved nutritional value.
XX Example 8; Page 71; 180pp; English.
XX 2 PCR primers (AAQ94968 and AAQ94969) were designed to prime replication

```

CC of plasmid pSK1, but excluding a 30 base fragment around the EarI site.
 CC pSK1 is a mutant of pBR322 in which the ampicillin gene has been deleted.
 CC PCR was performed using pSK1 as template. The product was utilised in the
 CC prodn. of pSK6 (see also AAQ94970-71), a vector used for the construction
 CC of genes (see AAQ94972-Q95005) coding for synthetic storage proteins
 CC (SSPs) (see AAR78236-59). These were expressed in the seeds of
 CC transformed soybean, rapeseed and corn to improve the lysine content
 XX
 SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGGTC 18
 ||| |||||
 Db 7 CGCTGCGCTCGGTC 20

RESULT 7
 AAV35805
 ID AAV35805 standard; DNA; 20 BP.
 XX AC AAV35805;
 XX 25-MAR-2003 (revised)
 DT 25-AUG-1998 (first entry)
 XX PCR primer used in the course of the invention.
 XX Dihydrodipicolinic acid synthase; DHDPS; chimeric gene;
 KW lysine inhibition; plant chloroplast transit sequence;
 KW plant seed-specific regulatory sequence; transgenic plant;
 KW increased lysine level; corn; Zea mays; soybean; Glycine max; PCR primer;
 KW ss.

XX Synthetic.
 OS US5773691-A.
 PN 30-JUN-1998.
 XX 07-JUN-1995; 95US-00474633.
 XX 19-MAR-1992; 92US-00855414.
 PR 18-MAR-1993; 93WO-US002480.
 PR 06-JAN-1994; 94US-00178212.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 FA Falco SC;
 PI WPI; 1998-387117/33.
 DR Chimeric genes encoding lysine production enzymes - useful for increasing
 PT transgenic seed lysine content without being inhibited by high levels of
 PT the amino acid.
 XX Example 21; Col 73; 106pp; English.

XX PCR primers AAV35805-06 were used to in the course of the invention. The
 CC specification describes a Corynebacterium daptA gene, which encodes a
 CC dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create
 CC chimeric genes of the invention. The chimeric genes contain a nucleic
 CC acid fragment encoding a DHDPS enzyme which is insensitive to inhibition
 CC by lysine operably linked to a plant chloroplast transit sequence and to
 CC a plant seed-specific regulatory sequence. The chimeric genes are useful
 CC for producing plants containing increased levels of lysine, especially in
 CC corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CGCGCGCTCGGTC 18
 ||| |||||
 Db 7 CGCTGCGCTCGGTC 20

RESULT 8
 AAV99501
 ID AAV99501 standard; DNA; 20 BP.
 XX AC AAV99501;
 XX 29-MAR-1999 (first entry)
 DT Plasmid pSK1 PCR primer SM70.
 DE Lysine; transgenic plant; seed storage protein; vector; pSK5; PCR;
 KW primer; ss.
 XX Synthetic.
 OS Escherichia coli.
 XX WO9842831-A2.
 PN 01-OCT-1998.
 XX 27-MAR-1998; 98WO-US006051.
 PR 27-MAR-1997; 97US-00824627.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 FA Falco SC, Mcdevitt RE, Epelbaum SU;
 PI WPI; 1999-045139/04.
 DR Nucleic acids and chimeric genes for increasing seed lysine content -
 PT comprise sequence encoding all or part of lysine ketoglutarate reductase,
 PT useful to improve nutritional quality of seeds from transformed plants.
 XX Example 21; Page 99; 231pp; English.
 PS PCR primers SM70 and SM71 (see AAV99502) are designed to remove the EarI
 CC site at base 2353 of plasmid pSK1, a spontaneous mutant of pBR322 in
 CC which the ampicillin gene and the EarI site near the gene are deleted.
 CC The product was used in the construction of expression vector pSK5.
 CC Chimeric genes for lysine-rich synthetic seed storage proteins suitable
 CC for expression in the seeds of plants have been constructed in pSK5 (see
 CC AAV99513-18, AAV99527-32, AAV99539-41). The invention also provides
 CC claimed nucleic acids and chimeric genes useful for improving the
 CC nutritional quality of seeds from transgenic plants. Methods involve
 CC manipulation of lysine ketoglutarate reductase and lysine-insensitive
 CC dihydrodipicolinic acid synthase activity (see AAW87757-66)
 XX Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CGCGCGCTCGGTC 18
 ||| |||||
 Db 7 CGCTGCGCTCGGTC 20

RESULT 9
 ADA16031
 ID ADA16031 standard; DNA; 20 BP.
 XX AC ADA16031;

```

XX 06-NOV-2003 (first entry)
DT
DE Plasmid pSK1 mutagenic PCR primer #1.
DE ss; lycC; transgenic; lysine accumulation;
KW dihydrodipicolinic acid synthase; DHDPs; lysine inhibition;
KW lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;
KW aspartokinase III; AKIII; synthetic seed storage protein; SSP.
KW
OS Synthetic.
OS
FN US6459019-B1.
XX
PD 01-OCT-2002.
XX
XX 24-MAR-1997; 97US-00823771.
XX
PR 19-MAR-1992; 92US-00855414.
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
FI Falco SC, Keeler SV, Rice JA;
XX
XX WPI; 2003-028272/02.
DR
XX
PT Transformed plants that accumulate lysine at higher levels in its seeds
PT than untransformed plants, has gene fragments encoding lysine-insensitive
PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX
PS Example 21; Col 76; 109pp; English.
XX
CC The invention relates to a plant comprising two foreign nucleotide
CC sequences which cause seeds obtained from the plant to accumulate lysine
CC at a level of at least 10% higher than seeds of a plant that do not
CC comprise the nucleotide, where the nucleotide comprises a fragment
CC encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive
CC to lysine inhibition, and a fragment encoding a plant lysine
CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment
CC is operably linked to a plant chloroplast transit sequence (CTS) and the
CC plant lysine ketoglutarate reductase subfragment is used in antisense
CC inhibition or cosuppression. Also included are progeny plants from the
CC above mentioned plant and seeds obtained from the above mentioned plant.
CC The seeds obtained from the above mentioned plant (e.g., rapeseed,
CC soybean or corn) comprising the foreign nucleic acid sequences accumulate
CC lysine at a higher level, preferably at a level of at least 10% higher
CC than seeds of a plant that do not comprise the foreign nucleic acid
CC sequences. Chimaeric gene comprising DHDPs from C. glutamicum and
CC aspartokinase III (from the lycC gene) of E. coli (mutated to be lysine-
CC insensitive) are also used to generate the above transgenic plants. Also
CC disclosed are synthetic seed storage proteins (SSP) used as an internal
CC source of lysine, built up from synthetic peptide monomers based around
CC an EarI site sequence (for generating multimeric proteins). The present
CC sequence is an oligonucleotide (or primer) used in the construction of
CC expression plasmids for expression of the chimaeric proteins or SSPs.
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 62.0%; Score 12.4; DB 8; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CCGCGCGCTCGGTC 18
DB 7 CCGCTCGGCTCGGTC 20
RESULT 10
ACH03677
ID ACH03677 standard; DNA; 20 BP.
XX

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AC ACH03677;
XX
DT 25-SEP-2003 (first entry)
XX
DE Plasmid pSK1 Ear I site mutagenic PCR primer #1.
XX
XX Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDPs;
KW seed lysine content; seed threonine content; seed storage protein; SSP;
KW chloroplast transit sequence; lysine-rich protein;
KW lysine ketoglutarate reductase; LKR; transgenic; ss; PCR; primer.
XX
OS Escherichia coli.
OS Synthetic.
XX
XX US2003056242-A1.
XX
XX 20-MAR-2003.
XX
XX 17-DEC-2001; 2001US-00023066.
XX
PR 19-MAR-1992; 92US-00855414.
PR 18-MAR-1993; 93WO-US002480.
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 24-MAR-1997; 97US-00823771.
XX
XX (FALC/) FALCO S C.
XX
XX Falco SC;
XX
XX WPI; 2003-521869/49.
DR
XX
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic
PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
PS Example 21; Page 41; 116pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPs) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimaeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimaeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimaeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monocot-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by EarI restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is an oligonucleotide used
CC in the preparation of a version of plasmid pSK1 used to clone the SSP
CC synthetic sequences
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

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Query Match 62.0%; Score 12.4; DB 9; Length 20;
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGGTC 18
 ||| |||||
 Db 7 CGCTGCGCTCGGTC 20

RESULT 11
 ADF73001/c
 ID ADF73001 standard; DNA; 20 BP.
 XX
 AC ADF73001;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Probe related to the invention #59.
 XX
 KW tubercle bacillus gene chip; ss; probe.
 XX
 OS Synthetic.
 XX
 PN CN1362526-A.
 XX
 PD 07-AUG-2002.
 XX
 PF 05-JAN-2001; 2001CN-00107010.
 XX
 PR 05-JAN-2001; 2001CN-00107010.
 XX
 PA (BAOL/) BAO L.
 XX
 PI Bao L, Zhang W, Wang X;
 XX
 DR WPI; 2003-240333/24.
 XX
 PT A tubercle bacillus gene chip useful for tuberculosis diagnosis and
 PT reasonable selection of medicine.
 XX
 PS Disclosure; SEQ ID NO 59; 4pp; Chinese.
 XX
 CC The present sequence represents a tubercle bacillus gene chip and its
 CC application. According to the characteristics of tubercle bacillus genome
 CC sequence and molecular mechanism produced by tubercle bacillus resistance
 CC to drug, and according to its application the probe can be designed and
 CC selected, and the probe array can be regularly and reasonable arranged
 CC according to a certain mode to form optimized probe array. The gene chip
 CC can be used for quickly, accurately and high-efficiency identifying
 CC tubercle bacillus, and can be used for screening and detecting its
 CC resistance to drug, and can detect the mutation of specific site of
 CC tubercle bacillus gene sequence and the mutation of non-specific site.
 CC The invention can be used for tuberculosis diagnosis and reasonable
 CC selection of medicine. The present sequence represents a probe related to
 CC the invention.
 XX
 SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 10; Length 20;
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCGGCGCTCGGTC 19
 ||| |||||
 Db 19 CGCGGCGCTCGGTC 6

RESULT 12
 AAD26768/c
 ID AAD26768 standard; DNA; 15 BP.
 XX
 AC AAD26768;

Query Match 59.0%; Score 11.8; DB 6; Length 15;
 Best Local Similarity 86.7%; Pred. No. 6.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCGGT 17
 ||| |||||
 Db 15 GSCGCGGCTCTCGGT 1

RESULT 13
 AAT61840/c
 ID AAT61840 standard; DNA; 17 BP.
 XX
 AC AAT61840;
 XX
 DT 08-MAY-1997 (first entry)
 XX
 DE Pseudomonas aeruginosa exoenzyme S gene antisense PCR primer.
 XX
 KW Exoenzyme S; exoS; detection; treatment; vaccination; infection;
 KW production; antibody; modification; ras protein; carcinoma; probe;
 KW mammalian; recombinant; primer; PCR; polymerase chain reaction; ss.
 XX
 OS Synthetic.

XX 09-APR-2002 (first entry)
 XX Human SNAP29 gene polymorphism detecting ASO primer #11.
 DE
 XX Human; synaptosomal-associated protein 29 kD; SNAP29 protein; primer;
 KW haplotyping; genotyping; membrane trafficking related disorder; ASO;
 KW gene therapy; polymorphism; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200190126-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016938.
 XX
 PR 23-MAY-2000; 2000US-0206529P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Kazemi A, Koshiy B, Tanguay DA;
 XX
 DR WPI; 2002-089916/12.
 XX
 CC Novel isolated polynucleotide, a polymorphic variant of synaptosomal-
 CC associated protein, 29 kD (SNAP29) gene useful for expressing SNAP29
 CC protein isoform to screen drugs to treat SNAP29 activity-related disease.
 CC
 PS Claim 16; Page 13; 115pp; English.
 XX
 CC The invention relates to genetic variants of human synaptosomal-
 CC associated protein, 29 kD (SNAP29) gene. The invention also relates to
 CC compositions and methods for haplotyping and/or genotyping the SNAP29
 CC gene in an individual. Polynucleotides of the invention are useful for
 CC studying the expression and function of SNAP29 and expressing SNAP29
 CC protein for use in screening candidate drugs to treat diseases related to
 CC SNAP29 activity. They are also used in gene therapy. The genotyping
 CC method is useful for determining if an individual has one of haplotype or
 CC haplotype pairs. The polymorphism and haplotype data is useful for
 CC validating whether SNAP29 is a suitable target for drugs to treat
 CC disorders related to membrane trafficking, screening for such drugs and
 CC reducing bias cells in clinical trials of such drugs. The present
 CC sequence is an allele-specific oligonucleotide (ASO) primer used to
 CC detect human SNAP29 gene polymorphisms
 XX
 SQ Sequence 15 BP; 3 A; 6 C; 5 G; 0 T; 0 U; 1 Other;

Query Match 59.0%; Score 11.8; DB 6; Length 15;
 Best Local Similarity 86.7%; Pred. No. 6.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCGGT 17
 ||| |||||
 Db 15 GSCGCGGCTCTCGGT 1

RESULT 13
 AAT61840/c
 ID AAT61840 standard; DNA; 17 BP.
 XX
 AC AAT61840;
 XX
 DT 08-MAY-1997 (first entry)
 XX
 DE Pseudomonas aeruginosa exoenzyme S gene antisense PCR primer.
 XX
 KW Exoenzyme S; exoS; detection; treatment; vaccination; infection;
 KW production; antibody; modification; ras protein; carcinoma; probe;
 KW mammalian; recombinant; primer; PCR; polymerase chain reaction; ss.
 XX
 OS Synthetic.

PN US5599665-A.
 XX
 PD 04-FEB-1997.
 XX
 PF 21-DEC-1993; 93US-00171299.
 XX
 PR 21-DEC-1993; 93US-00171299.
 XX
 PA (MCWR-) MCW RES FOUND INC.
 XX
 PI Kulich SM, Barbieri JT, Frank DW;
 XX
 DR WPI; 1997-118290/11.
 XX
 XX New isolated P. aeruginosa exo:enzyme S DNA - used to develop prods. for
 PT the detection, treatment and prevention of infections or for treating
 PT carcinoma(s).
 XX
 PS Disclosure; Col 19-20; 23pp; English.
 XX
 CC The present sequence is a PCR primer for the gene encoding the 49 kDa
 CC form of the Pseudomonas aeruginosa exoenzyme S (exoS), which can be used
 CC to detect, and in vaccines against P. aeruginosa infection. The protein
 CC can also be used to produce antibodies, which can be used to detect and
 CC treat P. aeruginosa infection, and modify ras protein function in
 CC mammalian carcinomas. The exoS gene can be used as a probe to detect P.
 CC aeruginosa infection, and in a vector for recombinant exoS production
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 3 G; 2 T; 0 U; 5 Other;
 Query Match 59.0%; Score 11.8; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. NO. 6.3e+04;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GGACGCGCGCTCGG 16
 Db :|||:|:|:|:|:|:|
 15 RGARGCGCCTSGG 1
 RESULT 14
 AAH23296
 ID AAH23296 standard; DNA; 19 BP.
 XX
 AC AAH23296;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Coding strand of binding site bsG.
 XX
 KW Nucleic acid binding polypeptide; repressor domain; cardiant; nootropic;
 KW circulatory active; anti-inflammatory; dermatological; neuroprotective;
 KW cerebroprotective; antibacterial; antifungal; antiviral; antirheumatic;
 KW osteopathic; gene therapy; zinc finger; binding site; ss.
 XX
 OS Synthetic.
 XX
 XX WO200153480-A1.
 XX
 XX 26-JUL-2001.
 XX
 PP 19-JAN-2001; 2001WO-GB0000202.
 XX
 PR 24-JAN-2000; 2000GB-00001582.
 PR 30-MAY-2000; 2000GB-00013102.
 PR 30-MAY-2000; 2000GB-00013103.
 PR 30-MAY-2000; 2000GB-00013104.
 XX
 XX (GEND-) GENDAQ LTD.
 XX
 XX Choo Y, Klug A, Moore M;
 XX
 DR WPI; 2001-451906/48.
 XX
 XX
 PT Nucleic acid binding polypeptide, used to identify nucleic acids and
 PT treat inflammatory, neurological, and dermatological disease, comprises a
 PT repressor domain and several nucleic acid binding domains linked by non-
 XX canonical linker(s).
 XX Example 9; Page 66; 142pp; English.
 PS
 CC The invention relates to a nucleic acid (NA) binding polypeptide (I)
 CC comprising a repressor domain and several NA binding domains (BDs) linked
 CC by at least one non-canonical linker. (I) may be used to identify NAs in
 CC a complex mixture, to differentiate single base pair changes in NAs, in
 CC the manufacture of chimeric restriction enzymes, to produce knock out
 CC organisms, and in the treatment of diseases such as: cardiovascular,
 CC inflammatory, metabolic, infectious, neurological, rheumatological,
 CC genetic, dermatological, and musculoskeletal diseases. The invented
 CC methods are used to produce novel NA binding polynucleotides and to
 CC modify existing NA binding polynucleotides comprising several NA BDs. The
 CC novel polypeptide comprises several nucleic acid binding domains linked
 CC by linker sequences. The invented polypeptide is therefore able to span
 CC longer or variable gaps, and a greater number of gaps, between DNA
 CC binding subsites. Sequences AAH23290-296 represent coding strand
 CC sequences of the binding sites used in gel shift experiments with
 CC peptides containing flexible linkers
 XX
 SQ Sequence 19 BP; 1 A; 5 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 59.0%; Score 11.8; DB 4; Length 19;
 Best Local Similarity 86.7%; Pred. NO. 6.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GGACGCGCGCTCGG 16
 Db |||||:|:|:|:|:|:|
 3 GGACGCGCGCTGGG 17
 RESULT 15
 AAH20644/c
 ID AAH20644 standard; DNA; 20 BP.
 XX
 AC AAH20644;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE Human telomeric repeat binding factor 2 oligonucleotide 111372.
 XX
 KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
 KW inhibitor; premature aging; hyperproliferative disorder; cancer;
 KW cyostatic; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20 b
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 FT modified_base 1..3 a
 FT /mod_base= OTHER
 FT /note= "2-O-methoxyethyl"
 FT modified_base 13..20 c
 FT /mod_base= OTHER
 FT /note= "2-O-methoxyethyl"
 XX
 PN WO200143752-A1.
 XX
 XX 21-JUN-2001.
 XX
 XX 14-DEC-2000; 2000WO-US033954.
 XX
 XX 17-DEC-1999; 99US-00467642.
 XX

PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowsert LM;
 XX
 DR WPI; 2001-398071/42.
 XX
 PT Antisense compounds targeted to nucleic acid encoding telomeric repeat
 binding factor 2 useful for treating conditions such as premature aging
 PT and diseases such as cancer.
 XX
 PS Claim 3; Page 80; 108pp; English.
 XX
 CC This invention describes a novel antisense compound (I) 8-30 nucleobases
 in length targeted to a polynucleotide encoding human telomeric repeat
 binding factor 2 (II) which specifically hybridizes with, and inhibits
 the expression of (II). (I) is useful for treating a human having a
 disease or condition associated with (II) such as premature aging or a
 hyperproliferative disorder especially cancer, by inhibiting the
 expression of (II) in human cells or tissues. (I) is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC The products of the invention have cytostatic activity. This sequence
 CC represents an antisense oligonucleotide used to illustrate the method of
 the invention
 XX
 SQ Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 5; Length 20;
 Best Local Similarity 86.7%; Pred. No. 6.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGTCA 19
 ||||| |||||
 Db 18 CGCGCGATCGGACA 4

Search completed: May 3, 2005, 19:48:37
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